<u>1</u> ∪	ORIGIN	SUMMARIES	
	FEATURES SOURCE	No. is the number of results predicted by chance to have a greater than or equal to the score of the result being printed, s derived by analysis of the total score distribution.	Pred. No. score gre and is de
Patent: US	JOURNAL	Mean 11.533; Variance 4.446; scale 2.594	Statistics:
Unknown. Unknown. Unclassifie 1 (bases 1 8ennett,A. Plant inhib	SOURCE ORGANISM REFERENCE AUTHORS TITLE	9enbank-new3 106:BCT 107:GEN1 108:GEN2 109:HTG1 110:HTG2 111:INV 112:MAM 113:VRT 114:PHG 115:PLN 116:PRI1 117:PRI2 118:ROD 119:SYN 120:UNA 121:VRL u-emb150_99 122:part1	Database: Database:
128278 Sequence 5 128278 g1819054	RESULT 1 LOCUS DEFINITION ACCESSION NID NED KEYWORDS	52:VRT4 53:PAT1 54:PAT2 55:PAT3 56:PAT4 57:PAT5 58:PHG 59:PLN1 60:PLN2 61:PLN3 62:PLN4 63:PLN5 64:PLN6 65:PLN7 66:PLN8 67:PLN9 68:PLN10 69:PLN11 70:PRI1 71:PRI2 72:PRI3 73:PRI4 74:PRI5 75:PRI6 76:PRI7 77:PRI8 78:PRI9 79:PRI10 80:PRI11 81:PRI12 82:PRI13 83:PRI14 84:PRI15 85:ROD1 86:ROD2 87:ROD3 88:ROD4 89:ROD5 90:ROD5 91:ROD7 92:ROD8 93:STR 94:SYN 95:UNA 96:VRL1 97:VRL2 98:VRL3 99:VRL4 100:VRL5 101:VRL6 102:VRL7 103:VRL8 104:VRL9 105:VRL10	
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		<pre>&gt;US-08-469-637A-1 (1-1527) from US08469637A.seq 1527 1 CGCCCAGCCGCCGCCTCCAATTCAACTGGAAAAAAAAAA</pre>	Title: Description: Perfect Score: N.A. Sequence: Comp:
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/organism="unknown" 15 a 8 c 25 g 26 t	1215	Location/Qualifiers	<pre>control fungal disease Patent: US 5569830-A 5 29-OCT-1996;</pre>	Plant inhibitors of fungal polygalacturonases and their use to	Bennett, A., Labavitch, J.M., Powell, A. and Stotz, H.	1 (bases 1 to 215)	Unclassified.	Unknown.	Unknown.	•	g1819054	128278	Sequence 5 from patent US 5569830.	128278 215 bp DNA	
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Eukaryotae; mitochondrial eukaryotes; Alveolata; hypotrichs; Stichotrichida; Oxytricha:
1 (bases 1 to 354)
Doak, T.G., Doerder, F.P., Jahn, C.L. and Herrick, G
A proposed superfamily of transposase genes: transposase genes:
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Bennett,A., Labavitch,J.M., Powell,A. and Stotz,H.
Plant inhibitors of fungal polygalacturonases and
control fungal disease
Patent: US 5569830-A 5 29-OCT-1996;
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Doak T.G., Doerder F.P., Jahn C.L., Herrick G.;
"A proposed superfamily of transposses genes: transposon-like elements in ciliated protozoa and a common 'D35E' motif";
Proc. Natl. Acad. Sci. U.S.A. 91:942-946(1994).
transposable elements trifallax";
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/db_xref="PID:g1881676"
/transl_table=6
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Oxytricha fallax
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                                                                                    Submitted (11-FEB-1997) School of Med. Rm5C334,
                                                                                                                                                  Unpublished
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[ bases 1 to 354)
                                                                                                               Direct Submission
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Doak, T.G., Williams, K.,
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/note="this is a bulk sequen
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/transposon="TBE1"
/note="this is a bulk sequence that was generated from
/note="this is a bulk sequence that was generated from
PCR product that represents many transposon templates"
                                    /organism="Oxytricha
/strain="9D1"
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/product="57kD zinc finger/protein
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/translation="HTRDLXKHLLKAHKKXXEXEXXXXXLKXLXKRKAREXXXXXXXX
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33; Mismatches 24
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13-MAR-1997 (Rel. 51, Created)
13-MAR-1997 (Rel. 51, Last updated, Version 1)
Oxytricha fallax 57kD zinc finger/protein chimera
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"A proposed superfamily of transposses genes: transposon-like elements in ciliated protozoa and a common 'D35E' motif";
proc. Natl. Acad. Sci. U.S.A. 91:942-946(1994).
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hypotrichs; Stichotrichida; Oxytrichidae; Oxytrio
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AXEXXXVXXXRNXLXSEXTKIMIKIQYKKIPVLAQIDLDTSLQSYLILEDSFDKKVIX
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Best Local Similarity 77.8%;
Matches 35; Conservative
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Sequence 354 BP; 106 A; 42 C; 4
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Local Similarity 23.7%;
es 23; Conservation
                                                                                                                                                        GAAGCTGCTCGAAGGTGAGGTTAGCATGTCCAATGTGCCGCTGCA 887
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                                  Carassius
L23876
g388622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cohen, I., Shani, Y. and Schwartz, M.
Cloning and characteristics of fish glial fibrillary acidic protein: implications for optic nerve regeneration
J. Comp. Neurol. 334 (3), 431-443 (1993)
93388923
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glial
Carassius
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        brain, mRNA
S66477
                                                                                       CRAGF1
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Vertebrata; Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Ostariophysi; Cypriniformes; Cyprinoidea; Cyprinidae; Cyprininae;
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fibrillary acidic
, mRNA Partial, 144
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/db_xref="plD:g435739"
/translation="VDLDVSKPDLTTALKEIRAOFEAMATSNMOETEEWYRSKFADLT
DAASRNTEALROAKOEANEYRROIQGLTCDLESLRGSNESLERGLREMEERFTIETAG
YODTVARLEBEIOMLKEEMARHLOEYODLLNVKLALDIEIATYRKLLEGEESRITVPV
ONFINLOFRDTSLDTKLTPEAHVKRSIVVRTVETRDGEIIKESTTERNDLP"
273 c 347 g 401 t
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   adult retina
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(GFAP-1) mRNA,
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dic protein (clone 2) [Cyprinus carpio-carp, 1441 nt]
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Pred. No. 3.26e-01;
38; Mismatches 36
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Pred. No. 3.26e-01
0; Mismatches 1
 cDNA to mRNA
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                                                                                              Direct Submission
Submitted (07-AUG-1992) G. Wiche, Institution of Vienna, Molecular Biology, University of Vienna,
                                                                                                                                                                                                                                                                                                                                           1 (bases 1 to 7095)

Zauner, W., Kratz, J., Staunton, J., Feick, P. and Wiche, G.

Identification of two distinct microtubule binding doma
recombinant rat MAP 1B

Care J. Cell Biol. 57 (1), 66-74 (1992)
                                                                                                                                                                                                                             Direct Submission
Submitted (07-AUG-1991) G. Wiche, Inst of Biochemistry,
of Vienna, Waehringerstrasse 17, 1090 Vienna, AUSTRIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Norway rat.
Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MAP1B gene; microtubule-associated
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R.norvegicus mRNA for microtubule associated X60370 X60371 X60550
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Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Ostariophysi; Cypriniformes; Cyprinoidea; Cyprinidae; Cyprininae;
                                                                                                                                                                        Wiche, G
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Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;
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Glasgow, E. and Schechter, N.
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/organism="Rattus norvegicus"
/strain="Sprague-Dawley"
/dev_stage="adult"
                                                          1..7095
                                                                        Location/Qualifiers
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IVVRTVETRDGEIIKESTTERKDLP"
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/taanslation="MGLNDRFASYIEKVRFLEQQNKNLVAELNQLRGKEPSRLGDIYQ
EELRELRQVDGLNAGKALEIERDNLASDLATLKQRLQEENALRQEAENNLRYFRQD
VDEAALNRYGVLERKIDALQDEISFLRKVHEBEMRQLQEQLIAQQVHVDLDVSKPDLTT
ALKEIRAQFEAMATSNMQETEEWYRSKFADLTDAAGRNAEALRQAKOEANEYRRQIQG
ATCDLESLRGSNESLERQLREMEERFAIETAGYQDTVARLEDEIQMLKEEMARHLQEY
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Pred. No. 3.26e-01;
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Local Similarity 76.1%;
hes 35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (01-JUL-1994) R.P. Hellens, John Innes Institute, Colney Lane, Norwich NR4 7UH, UK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished
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Charophyta/Embryophyta group; Embryophyta; Magnoliophyta;
Magnoliopsida; Rutanae; Sapindales; Fabaceae; Papilionoideae;
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Pisum sativum
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chalcone synthase; CHS-1A gene; CHS-1B
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QQGCFAGGTVLRLAKDLAENNKGARVLVVCSEITAVTFRGPSDTHLDSLVGQALFGDG
AAAVIVGSDPLPDVEKPLFELWTAQTIVPDSEGAIDGHLREAGLTFHLLKDVPSLVS
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ygene="CHS-1A"
join(1040..1217,1328..2319)
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1856 c 1799 g 1
                                                                                                                                                                                                                                                 GNMSSACVLFILDEMRRKSKEDGLATTGEGLEWGVLFGFGPGI
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                                                                                                                          join(<4336..4513,4642..>5633)
                                                                                                                                                             /gene="CHS-1A"
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                                                                                                                                                                                                                 /gene="CHS-1A"
                                                                                                                                                                                                                                                                                                                                                                                                              /codon_start=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone="B"
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                                     codon_start=1
                                                   _number="2.3.1.74"
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Pred. No. 1.38e+00;
0; Mismatches 11;
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AUTHORS
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AUTHORS
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (21-OCT-1996) Nematode Sequencing Project, Sanger Centre,
Hinxton, Cambridge CB10 1RQ, England and Department of Genetics,
Washington University, St. Louis, MO 63110, USA. E-mail:
jes@sanger.ac.uk or rw@nematode.wustl.edu

2E (bases 1 to 18632)
Wilson,R., Ainscough,R., Anderson,K., Baynes,C., Berks,M.,
Bonfield,J., Button,J., Conneell,M., Copsey,T., Cooper,J.,
Coulson,A., Craxton,M., Dear,S., Du,Z., Durbin,R., Favello,A.,
Fulton,L., Gardner,A., Green,P., Hawkins,T., Hillier,L., Jier,M.,
Johnston,L., Jones,M., Kershaw,J., Kirsten,J., Laister,N.,
Latreille,P., Lightning,J., Lloyd,C., McMurray,A., Morthmore,B.,
O'Callaghan,M., Parsons,J., Percy,C., Rifken,L., Roopra,A.,
Saunders,D., Shownkeen,R., Smaldon,N., Smith,A., Sonnhammer,E.,
Staden,R., Sulston,J., Theory MiegyJ., Thomas,K., Vaudin,M.,
Vaughan,K., Waterston,R., Watson,A., Weinstock,L.,
Valkinson-Sproat,J. and Wohldman,P.
Current sequence finishing criteria for the C. elegans genome sequencing consortium are that all bases are either sequenced unambiguously on both strands, or on a single strand with both a dye primer and dye terminator reaction, from distinct subclones. Exceptions are indicated by an explicit note. IMPORTANT: This sequence is NOT necessarily the entire insert of clone C29F3. It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between neighbouring submissions.

Coding sequences below are predicted from computer analysis, using the program Genefinder (P. Green, ms in preparation), and other
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryotae; mitochondrial eukaryotes; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida; Rhabditina; Rhabditc Rhabditidae; Peloderinae; Caenorhabditis.
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Similarity 81.6%;
31; Conservative
                                                                                                                                                                                                                                                                                                                                    Nature 368 (6466), 32-38 (1994)
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                                                                                                                                                                                                                                                                                                                                                                                          2 Mb of contiguous nucleotide sequence from chromosome III of
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QQGCFAGGTVLRLAKDLAENNKGARVLVVCSEITAVTFRGPSDTHLDSLVGQALFGDG
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KNIEKALVEAFQPLGISDINSLFWIAHPGGPAILDQVEAKLSLKQRKMQATRHVLSEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4514..4641
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Pred. No. 1.38e+00;
Wismatches 7;
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FEATURES
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TVNITSSNNKSAPVQAVDQMQNVEQVFSTKSESFYFVSNGGNIKLSTGNRKVOFFGSI
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HGKETTYSPVKYWLHRDPEQEAEFVEFLLENGESFTLTEKHLVFATDCQQNVKNLDDL
NPTSTGKINIGECFFMAQPEVRSSLYCV"
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6642..6740))
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RESTDRNIATVSAGEIVIGGEVYQUESQY
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8197..8292))
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                                                                                                                                                                                                                                                  complement(join(15422..15713,16068..16591,16640..17140,
                                                                                                                                                                                                                                                                                                                              ELSFNSTNLPPLNTTITFHGNFLHIEYYPNGTDSSKLFLNFDIEKSVTRSSEFFFACV
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13344..13893,13948..14262,14952..15141)
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                          /product="C29F3.a"
/db_xref="PID:e299496"
/db_xref="PID:g1813902"
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/db_xref="PID:e299268"
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/clone="C29F3"
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translation="MNETLDRVRLKRFLFYSYKFQLQSDQSVKAIVVMSGKPNSFVAG/
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Submitted (04-NOV-1996) Nematode Sequencing Project, Sanger Centre, Hinxton, Cambridge CB10 1RQ, England and Department of Genetics, Washington University, St. Louis, MO 63110, USA. E-mail:

jes@sanger.ac.uk or rw@nematode.wustl.edu
Order of segments is not known; 800 n's separate segments.
Order of segments is not known; 800 n's separate segments.
Cosmid=T09D4; Contig ID=00659; Length=42147; Status=Unfinished
Cosmid=T09D4; Contig ID=01673; Length=1019; Status=Unfinished
Cosmid=T09D4; Contig ID=01600; Length=1271; Status=Unfinished.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Caenorhabditis elegans.
Caenorhabditis elegans.
Caenorhabditis elegans.
Eukaryotae; mitochondrial eukaryotes; Metazoa; Nematoda;
Secernentea; Rhabditia; Rhabditida; Rhabditina; Rhabditoidea;
Rhabditidae; Caenorhabditis.
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HTGS; HTG
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Human DNA sequence *** SEQUENCING IN PROGRESS ***
799F10; HTGS phase 1.
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Similarity 90.0%;
27; Conservation
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IAVNIKKTLLGLPEVTLGIMPODGGTORLPKLTTVQNVLLDLTLIGKRIKANKIGI
VDRVIQPLGDGICTSTETTHKYLEEIAVOSAELANGKLINIDKGFVHNATQAVMTS
KEVLDNVILKMAKNKLIKLTNGNYPAPLKILDVVRTAYLDPKNGYEAEAKAFGELSOT
FOSKALFGLFEGSTNAKKNKYGKGLPVNEIAVVGAGFMCAGIANVTINKGIRTVLLDA
NQAGVERGQNHYATHLMRQLKROKISKLEREKIYNHLVPTIDYSAMKNNDVVIEAVFE
DLPLKHKVIRQIENVVGPNIIASNTSALPIKDIAAASSRSDKVIGMHYFSVVIEMQL
LEIITHDGTSKETLATAAQLGLKQGKLVVVVKCCPGFFVVRCLSPMKGEIVRLLOEDV
EPSELDKLTTKFGFPVGAATLADEAGLDVAEHVARYLGTALGPRVHGGSVDLLKSELVR
AGHKGEKTSKGIFYYCDGAKGSKKVNQEAAKLFEXYKLTPIKSYSSPEDRQLRLVSRF
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Pred. No. 1.38e+00;
0; Mismatches 3
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Homo sapiens

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RESULT 14
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formaldehyde dehydrogenase; ABC transporter; DNA ligase; DNA polymerase III alpha subunit; GumB protein; LysR transcriptional regulator; Mg-protoporhyrin IX; N-acetylornithine aminotransferase; NADH dehydrogenase subunit 4; NADH dehydrogenase subunit 5; acetate kinase; aspartoacylase(ASP); cation-transporting ATPase; cell division protein FtsH; chemotaxis protein ChaA; cytochrome oxidase division protein FtsH; chemotaxis protein ChaA; cytochrome oxidase bydrolase; dihydroflavonol 4-reductase; dihydropteroate pyrophosphorylase; esterase; ferrous iron transport protein B; fibrillh; formaldehyde dehydrogenase (glutathione); high light-inducible protein; leader peptidase I; lysostaphin; malonyl coenzyme A-acyl carrier protein transacylase; methyl-accepting chemotaxis protein (MCP); oligopeptide transport ATP-binding
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             D90904 150894 bp DNA BCT Synechocystis sp. PCC6803 complete genome, 6/27,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  * This sequence is unfinished. When sequencing is complete, 
* the sequence data presented in this record will be replac 
*by a single finished sequence with the same accession number.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                of segments is not known; sequence: BK799F10 Contic
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Vertebrata;
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Similarity 80.0%;
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/clone="799F10"
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No. 1.38e+00;
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38510 bp Unfinished
13742 bp Unfinished
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1000 bp Unfinished
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AUTHORS
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TITLE
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protein OppF; oxygen independent coprophorphyrinogen III oxidase; penicillin-binding protein 1B; phenoxybenzoate dloxygenase; phycocyanin a subunit; phycocyanin associated linker protein; phycocyanin b subunit; potassium channel; protein conferring resistance to acetazolamide, Zam; regulatory component of sensory transduction system; regulatory components of sensory transduction system; serine/threonine protein kinase; seryl-tRNA synthetase; servine/threonine protein kinase; seryl-tRNA synthetase.

Synthetase; sporulation protein SpoIID; sulfolipid biosynthesis protein SqdB; tRNA-Arg; tRNA-Leu; tyrosyl tRNA synthetase.

Synechocystis sp. (strain:PCC6803) DNA.

Synechocystis sp. (strain:PCC6803) DNA.

Enbacteria; Cyanobacteria; Chroococcales; Synechocystis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kaneko,T., Sato,S., Kotani,H., Tanaka,A., Asamizu,E., Nakamura,Y., Miyajima,N., Hirosawa,M., Sugiura,M., Sasamoto,S., Kimura,T., Hosouchi,T., Matsuno,A., Muraki,A., Nakazaki,N., Naruo,K., Okumura,S., Shimpo,S., Takeuchi,C., Wada,T., Watanabe,A., Yamada,M., Yasuda,M. and Tabata,S. Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. strain PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions DNA Res. 3 (3), 109-136 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Potential protein coding regions were assigned on the basis of similarity search of the ORFs and GeneMark analysis.

Location/Qualifiers
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Direct Submission
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GEIDTKRLKIRMELNSIEAIKNAVQSGLGAAFVSTTAIEKELENNVLHTAPIKNVEIR

RVLSVIINPNRYRSKASAAFIREVLPQFSTHPDALDPERLFANPYSSNNGDRQGDGKD
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/db_xref="PID:g1652227"
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                                                                                                                                                                                                                                                                                                    /product="hypothetical protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                            /note="ORF_ID:slr1019"
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                                                                                                                                                                                                                                                                 /transl_table=11
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Sg

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LYGGENLKSPGQVMGRTRGNRLTFFQGEISELLGKTVPVKITEARAFSLTGEALSLVT
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Aiampadkgqfrvfnqytelfsvgdlaqmvqkagadlglkveidhlenprveleehyf
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complement(438..5693)
/note-"ORF_ID:s110996"
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SLWLGRLASRPIAHLFKTFSQDVSTERVIGCTGTVTSKKLPYLANGTIGQAHVYDNAG
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DVSASISYRQEKHDGYESWFPTVTVKFKNKIVATLEGSESPMPIALLQITDMDRDNPY
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NLITISVSLPDWATVIPHHNQEILIIDQSPKGYGYLAIAKDSSDEDKWLKS"
complement(8962..10059)
                                                                                                                                                                                                                                                                                                                                                          RLKALLAEAGIDV"
                                                                                                                                                                                                                                                                                                                                                                                         KFELSAETLRVYYPDGRPFLSTVALATQAEQASQRANEEAQRAEREKLRAELAEAEND
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                                                                                                                                                                                /transl_table=1
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AUTHORS
TITLE
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AUTHORS
TITLE
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SOURCE
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MEDLINE
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Note: remainder of annotations omitted
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Best Local Similarity 81.6%;
Matches 31; Conservative
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Direct Submission

Submitted (06-MAY-1988) Cozzone A.J., University of Lyon,

Submitted (06-MAY-1988) Cozzone A.J., University of Lyon,

Submitted (06-MAY-1988) Cozzone A.J.,

Eaboratory of Molecular Biology, 43 Boulevard du onze Novembre,

69622 Villeurbanne, France

2 (bases 1 to 1344)

Rieul,C., Bleicher,F., Duclos,B., Cortay,J.C. and Cozzone,A.J.

Nucleotide sequence of the aceA gene coding for isocitrate lyas
                        Nucleotide sequence of the aceA gene co
Escherichia coli
Nucleic Acids Res. 16 (12), 5689 (1988)
88262573
                                                                                                                                                                                                                                                                                                                l (bases 1 to 1344)
Cozzone, A.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        aceA gene; isocitrate lyase; isocitritase
                                                                                                                                                                                                                                                                                                                                                                               Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                       Eubacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             coli aceA gene
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /translation="mkntwqtpdrtpdqeqfbtttenkniiteriisTqqiippqewy
bqbrpewvvttqgkaeiTybTgAvIStGqgbyttipArqkhrvTfTTHEppciwtath
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VQARGEQLRSGLAEIKNQYPTLFTEVRGWGLINGLEISAESSLTSVEIVKAAMEQGLL
LAPAGPKYLRFYPPLVYTEAEIAQAVEILRQAIATLV"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="hypothetical protein"
/db_xref="PID:g1652237"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note-"ORF_ID:slr1023"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /translation="MTYSPVVESVEAQAFAVTDLSPAAEFKTADFDTYVMNTYGRFPI
\IARGQGSTLWDTEGKSYLDFVAGIATCTLGHAHPALVRAVSDQIQKLHHVSNLYYIP
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/db_xref="PID:g1652236"
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/db_xref="PID:g1652235"
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Pred. No. 1.38e+00;
0; Mismatches 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOT 12-SEP-1993 for isocitrate lyase (EC 4.1.3.1).
                                                                                                                                                                                                                                                                                                                                                                                                       gamma subdivision;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 150894;
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                                                                                                                                                                                                                                                                                                                                                                                                       Enterobacteriaceae;
                                                                                                               isocitrate lyase in
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Search completed: Thu Aug 21 10:01:07 1997 Job time: 2597 secs.
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                                                                                                                  983 cttataactgctcgccgtcgttcaactggcagaaaaa 1019
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1488 CTTATTACTGCTTGCAGTAATTCAACTGGAAAAAAAA 1524
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Escherichia coli"
/strain="K12"
/map="91 min"
27..30
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/codon_start=1
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/db_xref="SWISS-PROT:P05313"
/transl_table=11
/transl_table=11
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10..1344
                                                                                                                                                                                                                                       Indels 0;
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